

The Disordered Structural Ensembles of Vasopressin and Oxytocin and Their Mutants

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SUPPLEMENTARY MATERIAL

Table S1-1: Dominant hydrogen bonds for sub-ensembles of native oxytocin.

<i>R_g</i> bounds	<i>Acceptor</i>	<i>Donor</i>	<i>Percent of sub-ensemble</i>
4.0-4.62 Å (compact)	Tyr ² -O	Asn ⁵ -NH	73.9%
	Tyr ² -O	Cys ⁶ -NH	68.2%
	Cys ⁶ -O	Gly ⁹ -NH	49.9%
	Gln ⁴ -OE1	Gln ⁴ -NH	15.1%
	Pro ⁷ -O	C terminus-NH1	14.3%
5.0-5.7 Å (extended)	Tyr ² -O	Asn ⁵ -NH	81.6%
	Tyr ² -O	Cys ⁶ -NH	78.6%

Table S1-2: Dominant hydrogen bonds for sub-ensembles of Q4T mutant of oxytocin.

<i>R_g</i> bounds	<i>Acceptor</i>	<i>Donor</i>	<i>Percent of sub-ensemble</i>
3.9-4.3 Å (compact)	Tyr ² -O	Asn ⁵ -NH	85.9%
	Tyr ² -O	Cys ⁶ -NH	84.2%
	Cys ⁶ -O	Gly ⁹ -NH	71.2%
	Pro ⁷ -O	C terminus-NH1	29.3%
	Cys ¹ -O	C terminus-NH2	12.7%
5.0-5.6 Å (extended)	Tyr ² -O	Asn ⁵ -NH	79.5%
	Tyr ² -O	Cys ⁶ -NH	83.5%

Table S1-3: Dominant hydrogen bonds for sub-ensembles of Q4T,P7G mutant of oxytocin.

<i>R_g bounds</i>	<i>Acceptor</i>	<i>Donor</i>	<i>Percent of sub-ensemble</i>
5.13-5.5 Å (extended)	Tyr ² -O	Asn ⁵ -NH	87.6%
	Tyr ² -O	Cys ⁶ -NH	72.7%
	Cys ⁶ -O	Gly ⁹ -NH	71.2%
	Asn ⁵ -OD1	Tyr ² -NH	10.2%

Table S1-4: Dominant hydrogen bonds for sub-ensembles of native vasopressin.

<i>R_g bounds</i>	<i>Acceptor</i>	<i>Donor</i>	<i>Percent of sub-ensemble</i>
4.1-4.43 Å (compact)	Tyr ² -O	Asn ⁵ -NH	92.2%
	Tyr ² -O	Cys ⁶ -NH	59.6%
	Pro ⁷ -O	C terminus-NH1	36.3%
	Cys ⁶ -O	Gly ⁹ -NH	31.1%
	Cys ¹ -O	C terminus-NH2	12.1%
	Pro ⁷ -O	Gly ⁹ -NH	11.0%
4.95-5.6 Å (extended)	Tyr ² -O	Asn ⁵ -NH	90.7%
	Tyr ² -O	Cys ⁶ -NH	63.5%
5.7-6.0 Å (extended)	Tyr ² -O	Asn ⁵ -NH	88.7%
	Tyr ² -O	Cys ⁶ -NH	41.5%
	Phe ³ -O	Cys ⁶ -NH	17.4%

Table S1-5: Dominant hydrogen bonds for sub-ensembles of Y2H mutant of vasopressin.

<i>R_g bounds</i>	<i>Acceptor</i>	<i>Donor</i>	<i>Percent of sub-ensemble</i>
4.0-4.48 Å (compact)	His ² -O	Asn ⁵ -NH	87.5%
	His ² -O	Cys ⁶ -NH	76.7%
	His ² -ND1	Gln ⁴ -NH	87.6%
	Pro ⁷ -O	C terminus-NH1	33.4%
	Cys ⁶ -O	Gly ⁹ -NH	30.7%
	Cys ¹ -O	C terminus-NH1	22.2%
4.85-5.67 Å (extended)	His ² -O	Asn ⁵ -NH	80.6%
	His ² -O	Cys ⁶ -NH	79.7%
	His ² -ND1	Gln ⁴ -NH	80.2%

Table S1-6: Dominant hydrogen bonds for sub-ensembles of Y2H+ mutant of vasopressin.

<i>R_g</i> bounds	<i>Acceptor</i>	<i>Donor</i>	<i>Percent of sub-ensemble</i>
4.2-4.48 Å (compact)	His ² -O	Asn ⁵ -NH	74.6%
	His ² -O	Cys ⁶ -NH	15.6%
	His ² -O	C terminus-NH ₂	62.6%
	Cys ⁶ -O	Gly ⁹ -NH	58.3%
	Gly ⁹ -O	Cys ⁶ -NH	54.8%
	Asn ⁵ -OD1	His ² -HD1	12.8%
5.45-6.25 Å (extended)	His ² -O	Asn ⁵ -NH	62.4%
	His ² -O	Cys ⁶ -NH	18.9%
	Asn ⁵ -OD1	His ² -HD1	35.7%

Table S1-7: Dominant hydrogen bonds for sub-ensembles of P7L mutant of vasopressin.

<i>R_g</i> bounds	<i>Acceptor</i>	<i>Donor</i>	<i>Percent of sub-ensemble</i>
4.5-4.9 Å (compact)	Tyr ² -O	Asn ⁵ -NH	31.9%
	Tyr ² -O	Cys ⁶ -NH	16.0%
	Asn ⁵ -OD1	Leu ⁷ -NH	22.8%
	Gln ⁴ -O	Arg ⁸ -NH	22.2%
	Phe ³ -O	Cys ⁶ -NH	18.9%
	Asn ⁵ -O	Arg ⁸ -NH	17.5%
	Phe ³ -O	Leu ⁷ -NH	17.0%
	Tyr ² -O	Cys ⁶ -NH	16.0%
	Phe ³ -O	Asn ⁵ -NH	13.44%
	Gln ⁴ -O	Leu ⁷ -NH	12.4%
5.0-5.5 Å (extended)	Tyr ² -O	Asn ⁵ -NH	41.4%
	Gln ⁴ -O	Leu ⁷ -NH	26.3%
	Phe ³ -O	Cys ⁶ -NH	22.1%
	Asn ⁵ -O	Arg ⁸ -NH	18.0%
5.7-6.1 Å (extended)	Tyr ² -O	Asn ⁵ -NH	44.2%

Table S2-1: Percentages of sub-ensembles of native oxytocin with specific DSSP¹ secondary structure. Blank entries imply 0.0%.

<i>R_g</i> bounds	<i>Residue</i>	<i>β-bridge</i>	<i>3₁₀ helix</i>	<i>Turn</i>
4.0-4.62 Å (compact)	1			
	2			
	3		2.6%	83.6%
	4		2.6%	85.1%
	5		2.6%	84.1%
	6	1.6%		
	7			67.6%
	8			67.5%
	9	1.6%		
5.0-5.7 Å (extended)	1			
	2			
	3		3.6%	92.0%
	4		3.6%	92.2%
	5		3.6%	91.2%
	6			
	7			1.0%
	8			
	9			

Table S2-2: Percentages of sub-ensembles of Q4T mutant of oxytocin with specific DSSP¹ secondary structure. Blank entries imply 0.0%.

<i>R_g</i> bounds	<i>Residue</i>	<i>3₁₀ helix</i>	<i>Turn</i>
3.9-4.3 Å (compact)	1		
	2		
	3	1.2%	98.3%
	4	1.2%	98.4%
	5	1.2%	98.4%
	6		1.9%
	7		90.4%
	8		90.5%
	9		
5.0-5.6 Å (extended)	1		
	2		
	3	1.6%	95.4%
	4	1.6%	95.8%
	5	1.6%	95.1%
	6		
	7		
	8		
	9		

Table S2-3: Percentages of sub-ensembles of Q4T,P7G mutant of oxytocin with specific DSSP¹ secondary structure. Blank entries imply 0.0%.

<i>R_g bounds</i>	<i>Residue</i>	<i>3₁₀ helix</i>	<i>α-helix</i>	<i>Turn</i>
5.13-5.5 Å (compact)	1			
	2			
	3	4.3%	12.8%	79.7%
	4	4.3%	12.8%	80.0%
	5	4.3%	12.8%	78.3%
	6		12.8%	13.0%
	7			11.8%
	8			1.0%
	9			

Table S2-4: Percentages of sub-ensembles of native vasopressin with specific DSSP¹ secondary structure. Blank entries imply 0.0%.

<i>R_g bounds</i>	<i>Residue</i>	<i>3₁₀ helix</i>	<i>Turn</i>
4.1-4.43 Å (compact)	1		
	2		
	3	8.7%	91.0%
	4	8.7%	91.0%
	5	8.7%	87.0%
	6		2.8%
	7		63.6%
	8		62.9%
	9		
4.95-5.6 Å (extended)	1		
	2		
	3	8.3%	91.6%
	4	8.3%	91.7%
	5	8.3%	88.2%
	6		1.0%
	7		1.0%
	8		
	9		
5.7-6.0 Å (extended)	1		
	2		
	3	23.1%	76.9%
	4	23.1%	76.9%
	5	23.1%	72.5%
	6		
	7		
	8		
	9		

Table S2-5: Percentages of sub-ensembles of Y2H mutant of vasopressin with specific DSSP¹ secondary structure. Blank entries imply 0.0%.

<i>R_g bounds</i>	<i>Residue</i>	<i>3₁₀ helix</i>	<i>Turn</i>
4.0-4.48 Å (compact)	1		
	2		
	3	1.0%	98.9%
	4	1.0%	98.8%
	5	1.0%	98.0%
	6		3.0%
	7		68.4%
	8		68.5%
	9		
4.85-5.67 Å (extended)	1		
	2		
	3	1.6%	97.7%
	4	1.6%	97.6%
	5	1.6%	96.4%
	6		1.6%
	7		1.6%
	8		
	9		

Table S2-6: Percentages of sub-ensembles of Y2H+ mutant of vasopressin with specific DSSP¹ secondary structure. Blank entries imply 0.0%.

<i>R_g bounds</i>	<i>Residue</i>	<i>Parallel β-bridge</i>	<i>Anti-parallel β-bridge</i>	<i>3₁₀ helix</i>	<i>Turn</i>
4.2-4.48 Å (compact)	1				
	2				
	3	7.2%		1.1%	86.7%
	4			1.1%	97.4%
	5			1.1%	55.0%
	6	7.2%	58.0%		
	7				77.3%
	8				77.3%
	9		58.0%		
5.45-6.25 Å (extended)	1				
	2		2.2%	2.6%	
	3	1.0%		3.4%	83.8%
	4			3.4%	90.8%
	5		2.2%	1.0%	58.5%
	6	1.0%			
	7				
	8				
	9				

Table S2-7: Percentages of sub-ensembles of P7L mutant of vasopressin with specific DSSP¹ secondary structure. Blank entries imply 0.0%.

<i>R_g</i> bounds	<i>Residue</i>	<i>Parallel β-bridge</i>	<i>Anti-parallel β-bridge</i>	<i>3₁₀ helix</i>	<i>α-helix</i>	<i>Turn</i>
4.5-4.9 Å (compact)	1					
	2		7.9%	3.5%		
	3	1.9%		3.5%	1.0%	47.8%
	4			5.3%	14.9%	60.3%
	5		7.6%	4.0%	19.4%	42.5%
	6	1.9%		4.3%	19.4%	34.6%
	7			3.2%	18.7%	34.7%
	8			1.1%	5.7%	22.0%
	9					
5.0-5.5 Å (extended)	1					
	2		1.0%	6.0%		
	3	1.0%		6.1%		47.3%
	4			12.9%	1.6%	76.7%
	5		1.0%	16.2%	1.8%	66.7%
	6	1.0%		17.3%	1.8%	42.3%
	7			12.0%	1.7%	29.0%
	8			1.6%		10.4%
	9					
5.7-6.0 Å (extended)	1					
	2		3.1%	1.0%		
	3			1.3%		57.4%
	4			2.6%		81.5%
	5		3.1%	2.2%		62.3%
	6			2.1%		19.8%
	7			1.0%		7.7%
	8					
	9					

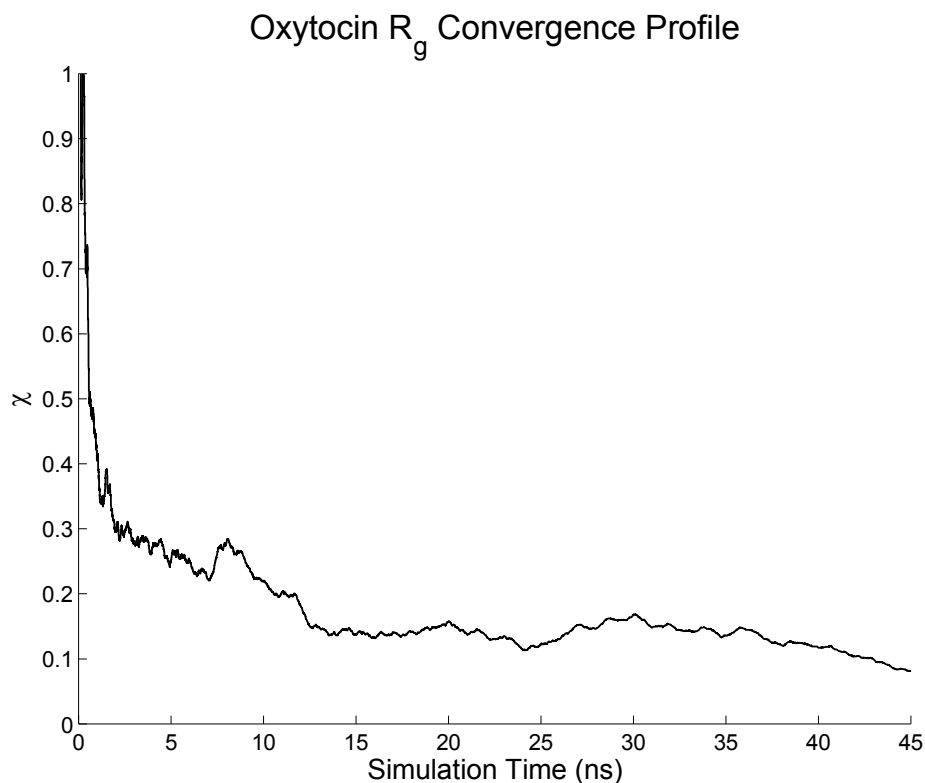
Table S3-1: The experimental and simulated chemicals shifts for native Oxytocin. Experimental values taken from Ohno *et al.*²

Residue	C_α		C_β		H_α		H_N	
	Exp	Sim	Exp	Sim	Exp	Sim	Exp	Sim
1	56.10	55.32	43.90	42.34	3.98	4.69		
2	58.10	57.59	39.10	39.62	4.85	4.67	8.23	8.58
3	62.50	63.00	39.00	37.77	4.16	3.80	7.88	7.51
4	58.00	56.71	28.70	28.98	4.13	4.16	8.21	7.44
5	53.40	53.83	38.60	39.75	4.75	4.74	8.33	7.91
6	54.50	52.88	41.50	42.15	4.85	5.03	8.23	7.91
7	63.50	63.08	32.10	32.24	4.46	4.44		
8	55.60	55.24	42.20	42.56	4.32	4.27	8.49	8.16
9	45.10	45.73			3.95	3.89	8.41	8.07

Table S3-2: The experimental and simulated chemicals shifts for native Oxytocin. Experimental values taken from Sikorska *et al.*³

Residue	C_α		C_β		H_α		H_N	
	Exp	Sim	Exp	Sim	Exp	Sim	Exp	Sim
1	52.55	55.09	40.04	42.56	4.20	4.71		
2	55.47	57.50	36.47	39.54	4.56	4.72	8.76	8.64
3	55.92	59.94	36.54	38.45	4.37	4.37	8.02	8.34
4	55.15	56.58	25.84	28.70	4.02	3.98	8.18	6.72
5	50.41	53.55	35.90	40.05	4.69	4.79	8.19	7.84
6	51.31	53.25	38.62	42.40	4.81	4.99	8.00	7.79
7	60.73	63.08	29.73	32.18	4.35	4.43		
8	53.80	56.24	27.98	30.84	4.20	4.22	8.49	8.27
9	42.28	45.71			3.82	3.90	8.28	8.11

Figure S1. Difference between the simulated R_g distributions of native oxytocin for two independent 45 ns production runs, showing the convergence of our simulations.



REFERENCES

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3. Sikorska, E.; Rodziewicz-Motowidło, S., Conformational studies of vasopressin and mesotocin using NMR spectroscopy and molecular modelling methods. Part I: Studies in water. *Journal of peptide science : an official publication of the European Peptide Society* **2008**, *14*, 76-84.